

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gregory Plowman  
Douglas Clary
- (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
Alk-7 RELATED DISORDERS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Lyon & Lyon  
(B) STREET: 633 West Fifth Street  
Suite 4700  
(C) CITY: Los Angeles  
(D) STATE: California  
(E) COUNTRY: U.S.A.  
(F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0  
(D) SOFTWARE: FastSEQ for Windows 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Filed herewith  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 60/044,428  
(B) FILING DATE: April 28, 1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Warburg, Richard J.  
(B) REGISTRATION NUMBER: 32,327  
(C) REFERENCE/DOCKET NUMBER: 234/118
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (213) 489-1600  
(B) TELEFAX: (213) 955-0440  
(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1793 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGCCACACT GACTAGAGCC AACC CGCGCAC TTCAAAAGGG TGTCGGTGCC GCGCTCCCCT 60  
CCCGCGGCCC GGGAACTTCA AAGCGGGCCG TGCTGCCCCG GCTGCCTCGC TCTGCTCTGG 120  
GGCCTCGCAG CCCC CGCGCGG GCCCGCTGGT GGCGATGACC CGGGCGCTCT GCTCAGCGCT 180  
CCGCCAGGCT CTCCTGCTGC TCGCAGCGGC CGCCGAGCTC TCGCCAGGAC TGAAGTGTGT 240  
ATGTCTTTTG TGTGATTCTT CAACTTTTAC CTGCCAAACA GAAGGAGCAT GTTGGGCATC 300  
AGTCATGCTA ACCAATGGAA AAGAGCAGGT GATCAAATCC TGTGTCTCCC TTCCAGAACT 360  
GAATGCTCAA GTCTTCTGTC ATAGTTCCAA CAATGTTACC AAAACCGAAT GCTGCTTCAC 420  
AGATTTTTTG AACAAACATAA CACTGCACCT TCCAACAGCA TCACCAAATG CCCC AAAACT 480  
TGGACCCATG GAGCTGGCCA TCATTATTAC TGTGCCGTGT TGCCTCCTGT CCATAGCTGC 540  
GATGCTGACA GTATGGGCAT GCCAGGGTCG ACAGTGCTCC TACAGGAAGA AAAAGAGACC 600  
AAATGTGGAG GAACCACTCT CTGAGTGCAA TCTGGTAAAT GCTGGAAAAA CTCTGAAAGA 660  
TCTGATTATG GATGTGACCG CCTCTGGATC TGGCTCTGGT CTACCTCTGT TGGTTCAAAG 720  
GACAAATTGCA AGGACGATTG TGCTTCAGGA AATAGTAGGA AAAGGTAGAT TTGGTGAGGT 780  
GTGGCATGGA AGATGGTGTG GGGAAGATGT GGCTGTGAAA ATATTCTCCT CCAGAGATGA 840  
AAGATCTTGG TTTCTGTAGG CAGAAATTTA CCAGACGGTC ATGCTGCGAC ATGAAAACAT 900  
CCTTGTTTTT ATTGCTGCTG ACAACAAAGA TAATGGAAT TGGACTCAAC TTTGGCTGGT 960  
ATCTGAATAT CATGAACAGG GCTCCTTATA TGACTATTTG AATAGAAATA TAGTGACCGT 1020  
GGCTGGAATG ATCAAGCTGG CGCTCTCAAT TGCTAGTGGT CTGGCACACC TTCATATGGA 1080  
GATTGTTGGT ACACAAGGTA AACCTGCTAT TGCTCATCGA GACATAAAAT CAAAGAATAT 1140  
CTTAGTGAAA AAGTGTGAAA CTTGTGCCAT AGCGGACTTA GGGTTGGCTG TGAAGCATGA 1200  
TTCAATACTG AACACTATCG ACATACCTCA GAATCCTAAA GTGGGAACCA AGAGGTATAT 1260  
GGCTCCTGAA ATGCTTGATG ATACAATGAA TGTGAATATC TTTGAGTCCT TCAAACGAGC 1320  
TGACATCTAT TCTGTTGGTC TGGTTTACTG GGAAATAGCC CGGAGGTGTT CAGTCGGAGG 1380  
AATTGTTGAG GAGTACCAAT TGCCTTATTA TGACATGGTG CCTTCAGATC CCTCGATAGA 1440  
GGAAATGAGA AAGGTTGTTT GTGACCAGAA GTTTCGACCA AGTATCCCAA ACCAGTGGCA 1500  
AAGTTGTGAA GCACTCCGAG TCATGGGGAG AATAATGCGT GAGTGTGGT ATGCCAACGG 1560  
AGCGGCCCCG CTAAGTCTC TTCGTATTAA GAAGACTATA TCTCAACTTT GTGTCAAAGA 1620  
AGACTGCAAA GCCTAATGAT GATAATTATG TTAAAAAGAA ATCTCTCATA GCTTTCTTTT 1680  
CCATTTTCCC CTTTATGTGA ATGTTTTTTC CATTTTTTTT TTGTTCTACC TCAAAGATAA 1740  
GACAGTACAG TATTTAAGTG CCCATAAGGC AGCATGAAAA GATAACTCTA AAG 1793

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Arg Ala Leu Cys Ser Ala Leu Arg Gln Ala Leu Leu Leu Leu  
1 5 10 15  
Ala Ala Ala Ala Glu Leu Ser Pro Gly Leu Lys Cys Val Cys Leu Leu  
20 25 30

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Cys	Asp	Ser	Ser	Asn	Phe	Thr	Cys	Gln	Thr	Glu	Gly	Ala	Cys	Trp	Ala	
	35						40					45				
Ser	Val	Met	Leu	Thr	Asn	Gly	Lys	Glu	Gln	Val	Ile	Lys	Ser	Cys	Val	
	50					55					60					
Ser	Leu	Pro	Glu	Leu	Asn	Ala	Gln	Val	Phe	Cys	His	Ser	Ser	Asn	Asn	
65					70					75					80	
Val	Thr	Lys	Thr	Glu	Cys	Cys	Phe	Thr	Asp	Phe	Cys	Asn	Asn	Ile	Thr	
				85					90					95		
Leu	His	Leu	Pro	Thr	Ala	Ser	Pro	Asn	Ala	Pro	Lys	Leu	Gly	Pro	Met	
			100					105					110			
Glu	Leu	Ala	Ile	Ile	Ile	Thr	Val	Pro	Val	Cys	Leu	Leu	Ser	Ile	Ala	
		115					120					125				
Ala	Met	Leu	Thr	Val	Trp	Ala	Cys	Gln	Gly	Arg	Gln	Cys	Ser	Tyr	Arg	
	130					135					140					
Lys	Lys	Lys	Arg	Pro	Asn	Val	Glu	Glu	Pro	Leu	Ser	Glu	Cys	Asn	Leu	
145					150					155					160	
Val	Asn	Ala	Gly	Lys	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Val	Thr	Ala	
				165					170					175		
Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	
			180					185					190			
Arg	Thr	Ile	Val	Leu	Gln	Glu	Ile	Val	Gly	Lys	Gly	Arg	Phe	Gly	Glu	
		195					200					205				
Val	Trp	His	Gly	Arg	Trp	Cys	Gly	Glu	Asp	Val	Ala	Val	Lys	Ile	Phe	
	210					215					220					
Ser	Ser	Arg	Asp	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	
225					230					235					240	
Thr	Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	
				245					250					255		
Asn	Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Glu	Tyr	
			260					265					270			
His	Glu	Gln	Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Asn	Arg	Asn	Ile	Val	Thr	
		275					280					285				
Val	Ala	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala	
	290					295					300					
His	Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	
305					310					315					320	
His	Arg	Asp	Ile	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Cys	Glu	Thr	
				325					330					335		
Cys	Ala	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Lys	His	Asp	Ser	Ile	Leu	
			340					345					350			
Asn	Thr	Ile	Asp	Ile	Pro	Gln	Asn	Pro	Lys	Val	Gly	Thr	Lys	Arg	Tyr	
		355					360					365				

Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu  
 370 375 380

Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu  
 385 390 395 400

Ile Ala Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu Tyr Gln Leu  
 405 410 415

Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg  
 420 425 430

Lys Val Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro Asn Gln Trp  
 435 440 445

Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys  
 450 455 460

Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys  
 465 470 475 480

Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala  
 485 490

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 6 and 7 stand  
 for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

His Arg Asp Leu Lys Xaa Xaa Asn  
 1 5

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.  
 The letter "N" stands for Inosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GARRARGTNG CNGTNAARRT NTT

23

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.  
The letter "N" stands for Inosine.  
The letter "K" stands for G or T.  
The letter "M" stands for A or C.  
The letter "Y" stands for C or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTRATRTCNC KRTGNGMNAT NGMNGGYTT

29

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 2 stands for Lys or  
Glu. "Xaa" in position 7 stands for  
Val or Ile.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Xaa Val Ala Val Lys Xaa Phe  
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TTCCAGCCAC GGTCACATATG TT

22

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Tyr Arg Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTTCGAAAGC TTGAAATCGG TACCATCGAT TCTAGAGTTA ACTTCGAA

48

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCTAGAACG CGTTAAGGCG CGCCAATATC GATGAATTCT TCGAAGC

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